

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 30, 2002, 11:49:01 ; Search time 18.17 Seconds
(without alignments)
26.232 Million cell updates/sec

Title: US-09-432-546-4

Sequence: 1 RRPMPWMPKMWPLI 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 segs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	62	62.6	144 1	INDC_BOVIN
2	52	52.5	1112 1	CN3B_HUMAN
3	51.5	52.0	492 1	ADRO_BOVIN
4	51	51.5	1173 1	VG12_CVH22
5	50.5	51.0	278 1	RCEL_RHOGE
6	50.5	51.0	494 1	ADRO_RAT
7	49.5	50.0	253 1	Y945_MYCTV
8	49.5	50.0	491 1	ADRO_HUMAN
9	48.5	49.0	212 1	PR12_PIG
10	48.5	49.0	228 1	PR12_PIG
11	48	48.5	990 1	ENV_OMVVS
12	47	47.5	942 1	ENV_CAEVG
13	47	47.5	966 1	ENV_CAEVG
14	47	47.5	982 1	ENV_VILV
15	47	47.5	983 1	ENV_VILV
16	47	47.5	989 1	ENV_VILV
17	47	47.5	991 1	ENV_VILV
18	46	46.5	533 1	UBIB_PSEAF
19	46	46.5	572 1	GA6_IPHA
20	45.5	46.0	660 1	FAGB_ECOLI
21	45	45.5	115 1	NUPM_BOVIN
22	45	45.5	115 1	NUPM_BOVIN
23	45	45.5	115 1	NUPM_BOVIN
24	45	45.5	115 1	NUPM_BOVIN
25	45	45.5	115 1	NUPM_BOVIN
26	44	44.4	115 1	NUPM_BOVIN
27	44	44.4	407 1	FUCO_CABEL
28	44	44.4	485 1	ADRO_BOVIN
29	44	44.4	488 1	ADRO_BOVIN
30	44	44.4	489 1	ADRO_BOVIN
31	44	44.4	492 1	ADRO_BOVIN
32	44	44.4	492 1	ADRO_BOVIN
33	44	44.4	492 1	ADRO_BOVIN

34	44	44.4	493 1	ADRO_BOVIN
35	44	44.4	543 1	ADRO_BOVIN
36	44	44.4	655 1	ADRO_BOVIN
37	44	44.4	984 1	ADRO_BOVIN
38	43.5	43.9	515 1	ADRO_BOVIN
39	43.5	43.9	515 1	ADRO_BOVIN
40	43.5	43.9	515 1	ADRO_BOVIN
41	43.5	43.9	515 1	ADRO_BOVIN
42	43.5	43.9	515 1	ADRO_BOVIN
43	43.5	43.9	515 1	ADRO_BOVIN
44	43.5	43.9	515 1	ADRO_BOVIN
45	43.5	43.9	515 1	ADRO_BOVIN

ALIGNMENTS

RESULT	ID	INDC_BOVIN	STANDARD	PRT	144 AA.
AC	P33046	INDC_BOVIN	STANDARD	PRT	144 AA.
DT	01-OCT-1993	(Rel. 27, Created)			
DT	01-OCT-1993	(Rel. 27, Last sequence update)			
DT	01-NOV-1997	(Rel. 35, Last annotation update)			
DE	INDOLICIDIN PRECURSOR.				
OS	Bos taurus (bovine)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Bone marrow;				
RA	MEDLINE=92393368; PubMed=1520337;				
RA	del Sal G., Storici P., Schneider C., Romeo D., Zanetti M.;				
RL	"CDNA cloning of the neutrophil bactericidal peptide indolicidin.";				
RL	Biochem. Biophys. Res. Commun. 187:467-472(1992).				
RP	[2]				
RC	SEQUENCE OF 131-143.				
RA	TISSUE=Neutrophils;				
RA	Medline=92165771; PubMed=1537821;				
RA	Selsted M.E., Novotny M.J., Morris W.L., Tang Y.-Q., Smith W.;				
RT	Cullor J.S.;				
RT	"Indolicidin, a novel bactericidal tridecapeptide amide from				
RL	neutrophils.";				
CC	J. Biol. Chem. 267:4292-4295(1992).				
CC	-1- FUNCTION: POTENT MICROBICIDAL ACTIVITY, ACTIVE AGAINST				
CC	STAPHYLOCOCCUS AUREUS AND ESCHERICHIA COLI.				
CC	-1- TISSUE SPECIFICITY: LARGE GRANULES OF NEUTROPHILS.				
CC	-1- PM: ELASTASE MIGHT BE RESPONSIBLE FOR ITS MATURATION.				
CC	-1- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.				
CC	-----				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: X67340; CAA47755.1; -				
DR	PIR: JCI222; JC1222.				
DR	PIR: A42387; A42387.				
DR	InterPro: IPR001894; Cathelicidin.				
DR	Pfam: PF00666; Cathelicidins; 1.				
DR	ProDom: PD001838; Cathelicidins; 1.				
DR	PROSITE: PS00946; CATHELICIDINS_1; 1.				
DR	PROSITE: PS00947; CATHELICIDINS_2; 1.				
KW	Antibiotic; Amidation; Signal.				
FT	STGNAL	1	29	POTENTIAL.	
FT	PROPEP	30	130	INDOLICIDIN.	
FT	PEPTIDE	131	143	PYRROLIDONE CARBOXYLIC ACID (BY	
FT	MOD_RES	30	30		

FT DISULFID 85 96 SIMILARITY.
 FT DISULFID 107 124 BY SIMILARITY.
 FT MOD.RES 143 143 AMIDATION (G-144 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 144 AA, 16479 MW, E3B1CBEB55C09911 CRC64;

Query Match 62.6%; Score 62; DB 1; Length 144;
 Best Local Similarity 75.0%; Pred. No. 0.088;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 RWPMPMK 9
 Db 135 KWPMPMR 142

RESULT 2
 CN3B_HUMAN STANDARD; PRT: 1112 AA.
 ID Q1370; Q00639; Q14408;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 20-APR-2001 (Rel. 40, Last annotation update)
 DE CGMP-INHIBITED 3',5'-CYCLIC PHOSPHODIESTERASE B (EC 3.1.4.17) (CYCLIC
 DE GMP INHIBITED PHOSPHODIESTERASE B) (CGI-PDE.B) (CGIPDE1) (CGIP1).
 GN PDE3B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fat;
 EX MEDLINE=97038690; PubMed=8884271;
 RA Miki T., Taira M., Hockman S., Shimada F., Lieman J., Napolitano M.,
 RA Ward D., Taira M., Makino H., Manganiello V.C.;
 RT "Characterization of the cDNA and gene encoding human PDE3B, the
 RT cGMP isoform of the human cyclic GMP-inhibited cyclic nucleotide
 RT phosphodiesterase family.";
 RL Genomics 36:476-485(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97079687; PubMed=8921398;
 RA Loebbert R.W., Winterpacht A., Seipel B., Zabel B.U.;
 RT "Molecular cloning and chromosomal assignment of the human homologue
 RT of the rat cGMP-inhibited phosphodiesterase 1 (PDE3A) -- a gene
 RT involved in fat metabolism located at 11p15.1.";
 RL Genomics 37:211-218(1996).
 RN [3]
 RP FUNCTION: MAY PLAY A ROLE IN FAT METABOLISM.
 CC -1 CATALYTIC ACTIVITY: GUANOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =
 CC GUANOSINE 5'-PHOSPHATE.
 CC -1 ENZYME REGULATION: INHIBITED BY CGMP.
 CC -1 SUBCELLULAR LOCATION: MEMBRANE-BOUND (POTENTIAL).
 CC -1 TISSUE SPECIFICITY: ABUNDANT IN ADIPOSE TISSUES.
 CC -1 SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL; U38178; AAC50724.1; -;
 DR EMBL; D50640; BAA09306.1; JOINED.
 DR EMBL; D50645; BAA09306.1; JOINED.
 DR EMBL; D50626; BAA09306.1; JOINED.
 DR EMBL; D50627; BAA09306.1; JOINED.
 DR EMBL; D50628; BAA09306.1; JOINED.
 DR EMBL; D50629; BAA09306.1; JOINED.
 DR EMBL; D50630; BAA09306.1; JOINED.

DR EMBL; D50631; BAA09306.1; JOINED.
 DR EMBL; D50632; BAA09306.1; JOINED.
 DR EMBL; D50633; BAA09306.1; JOINED.
 DR EMBL; D50634; BAA09306.1; JOINED.
 DR EMBL; D50635; BAA09306.1; JOINED.
 DR EMBL; D50637; BAA09306.1; JOINED.
 DR EMBL; D50638; BAA09306.1; JOINED.
 DR EMBL; D50639; BAA09306.1; JOINED.
 DR EMBL; X95520; CAA64774.1; -;
 DR MIM; 602047; -;
 DR InterPro; IPR005607; HDC.
 DR InterPro; IPR002073; PDEase.
 DR Pfam; PF00233; PDEase; 1.
 DR SMART; SM00471; HDC; 1.
 DR PROSITE; PS00126; PDEASE_I; 1.
 KM Hydrolyase; CGMP; Membrane.
 FT DOMAIN 1077 1080 POLY-GU.
 FT CONFLICT 84 84 D -> A (IN REF. 2).
 FT CONFLICT 87 87 A -> V (IN REF. 2).
 SQ SEQUENCE 1112 AA, 124376 MW, E5141C3DA12E9B0 CRC64;

Query Match 52.5%; Score 52; DB 1; Length 1112;
 Best Local Similarity 62.5%; Pred. No. 9.6;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 WPMWPMK 10
 Db 169 WQWMSMP 176

RESULT 3
 ADRO_BOVIN STANDARD; PRT: 492 AA.
 ID ADRO_BOVIN
 AC P08165;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE NADH:ADRENODOXIN OXIDOREDUCTASE, MITOCHONDRIAL PRECURSOR
 DE (EC 1.18.1.2) (ADRENODOXIN REDUCTASE) (AR) (FERREDOXIN-NADP(+)
 DE REDUCTASE).
 GN FDXR OR ADRX.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_Taxid=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 CC MEDLINE=94177140; PubMed=8130767;
 RA Takata Y., Sagara Y., Kono A., Sekimizu K., Horiuchi T.;
 RT "Gene structure of bovine adrenodoxin reductase.";
 RL Biol. Pharm. Bull. 16:1200-1206(1993).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 CC MEDLINE=8198050; PubMed=3448086;
 RA Sagara Y., Takata Y., Miyata T., Hara T., Horiuchi T.;
 RT "Cloning and sequence analysis of adrenodoxin reductase cDNA from
 RT bovine adrenal cortex.";
 RL J. Biochem. 102:1333-1336(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 CC MEDLINE=87270696; PubMed=3038094;
 RA Nonaka Y., Murakami H., Yabusaki Y., Kuramitsu S., Kagamiyama H.,
 RA Yamano T., Okamoto M.;
 RT "Molecular cloning and sequence analysis of full-length cDNA for mRNA
 RT of adrenodoxin oxidoreductase from bovine adrenal cortex.";
 RL Biochem. Biophys. Res. Commun. 145:1239-1247(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Adrenal cortex;
 RX MEDLINE=89170752; PubMed=2924777;
 RA Hanukoglu I., Guttinger T.;

FT CARBOHYD 930 930 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1015 1015 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1020 1020 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1037 1037 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1049 1049 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1061 1061 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1066 1066 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1076 1076 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1082 1082 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1096 1096 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1173 1173 AA; 128639 MW; B9CA9A4A796B3BD CRC64;
 SO SEQUENCE

Query Match 51.5%; Score 51; DB 1; Length 1173;
 Best Local Similarity 71.4%; Pred: No. 13; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 1;
 OY 2 RMPWPM 8
 DB 1113 KMPWPM 1119

RESULT 5
 RCBL_RHOGE STANDARD; PRT; 278 AA.
 ID RCBL_RHOGE
 AC P51760;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE REACTION CENTER PROTEIN L CHAIN (PHOTOSYNTHETIC REACTION CENTER L SUBUNIT).
 GN PUF.
 OS Rhodococcus gelatinosus (Rhodopseudomonas gelatinosa).
 OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;
 OC RUDRIVIVAX
 NC NCB1_Taxid-28068;
 RN RX
 RP SEQUENCE FROM N.A.
 RC STRAIN-1144;
 RX MEDLINE-94132007; PubMed-8300574;
 RA Matsushima K.V.P., Matsura K., Ohshima S., Shimada K.;
 RT "Primary structure and transcription of genes encoding B870 and photosynthetic reaction center apoproteins from Rudriviavax gelatinosus";
 RT J. Biol. Chem. 269:2477-2484(1994).
 RN RP
 RP SEQUENCE FROM N.A.
 RC STRAIN-51;
 RX MEDLINE-97033541; PubMed-8879238;
 RA Ouchane S., Picaud M., Reiss-Husson F., Vernotte C., Astier C.;
 RT "Development of gene transfer methods for Rudriviavax gelatinosus S1: construction, characterization and complementation of a puf operon deletion strain";
 RT Mol. Gen. Genet. 252:379-385(1996).
 RL
 RL -1- FUNCTION: THE REACTION CENTER IS A MEMBRANE-BOUND COMPLEX THAT MEDIATES THE INITIAL PHOTOCHEMICAL EVENT IN THE ELECTRON TRANSFER PROCESS OF PHOTOSYNTHESIS.
 CC -1- SUBUNIT: REACTION CENTER IS COMPOSED OF FOUR BACTERIOCHLOROPHYLLS, TWO BACTERIOPEOPHYTINS, TWO UBIQUINONES, ONE IRON, AND THREE HIGHLY HYDROPHOBIC POLYPEPTIDE CHAINS (DESIGNATED L, M, AND H).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE REACTION CENTER L/M CHAINS / PSBA / PSBD FAMILY.
 CC
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 CC
 CC EMBL, D16822; BAA04100.1; -

DR EMBL: U30310; AAA73927.1; -
 DR EMBL: U51298; ABA1576.1; -
 DR HSSP: P02934; 2RCR
 DR InterPro: IPR000484; Photo_RC.
 DR Pfam: PF00124; Photoc. 1
 DR PRINTS: PR00256; REACTCENTRE.
 DR PRODOM: PD000551; Photo_RC; 1.
 DR PROSITE: PS00244; REACTION_CENTER; 1.
 DR Transmembrane: Electron transport; Photosynthesis; Reaction center; Iron; Magnesium.
 KM Iron; Magnesium.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT TRANSMEM 32 55 POTENTIAL.
 FT TRANSMEM 84 112 POTENTIAL.
 FT TRANSMEM 115 140 POTENTIAL.
 FT TRANSMEM 170 199 POTENTIAL.
 FT TRANSMEM 225 251 POTENTIAL.
 FT METAL 173 173 POTENTIAL. (BACTERIOCHLOROPHYLL B) (BY SIMILARITY).
 FT METAL 190 190 IRON (NON HAEM) (BY SIMILARITY).
 FT METAL 230 230 IRON (NON HAEM) (BY SIMILARITY).
 FT BINDING 216 216 QUINONE B (BY SIMILARITY).
 FT CONFLICT 278 278 K -> N (IN REF. 2).
 SO SEQUENCE 278 AA; 31210 MW; 0ACFC1241890DC5 CRC64;

Query Match 51.0%; Score 50.5; DB 1; Length 278;
 Best Local Similarity 42.9%; Pred: No. 4.3; Indels 9; Gaps 2;
 Matches 9; Conservative 1; Mismatches 2;
 OY 1 RRWP-WPM-----KMP 12
 DB 257 RGWPEWGMWMLNLPINSOWPL 277

RESULT 6
 ADRO_RAT STANDARD; PRT; 494 AA.
 ID ADRO_RAT
 AC P56522;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE NADPH:ADRENODOXIN OXIDOREDUCTASE, MITOCHONDRIAL PRECURSOR (EC 1.18.1.2) (ADRENODOXIN REDUCTASE) (AR) (FERREDOXIN-NADP(+)-REDUCTASE).
 GN FDXR
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_Taxid-10116;
 RN RX
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-54.
 RC STRAIN-NISTAR; TISSUE-Adrenal gland;
 RX MEDLINE-99454627; PubMed-10525147;
 RA Sagara Y., Watanabe Y., Kodama H., Aramaki H.;
 RT "cDNA cloning, overproduction and characterization of rat adrenodoxin reductase";
 RT Biochim. Biophys. Acta 1434:284-295(1999).
 RL
 RL -1- FUNCTION: SERVES AS THE FIRST ELECTRON TRANSFER PROTEIN IN ALL THE MITOCHONDRIAL P450 SYSTEMS, INCLUDING CHOLESTEROL SIDE CHAIN CLEAVAGE IN ALL STEROIDAL TISSUES, STEROID 11-BETA HYDROXYLATION IN THE ADRENAL CORTEX, 25-OH-VITAMIN D3-24 HYDROXYLATION IN THE KIDNEY, AND STEROL C-27 HYDROXYLATION IN THE LIVER.
 CC -1- CATALYTIC ACTIVITY: REDUCED ADRENODOXIN + NADP(+) = OXIDIZED ADRENODOXIN + NADPH.
 CC -1- COFACTOR: FAD.
 CC -1- PATHWAY: CHOLESTEROL SIDE-CHAIN-CLEAVAGE SYSTEM.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
 CC
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DR EMBL: D63761: BAA23759.1; -
DR InterPro: IPR000759; Adtrnx_redctse.
DR PRINTS: PR00419; ADXRDYASE.
KM Electron transport; Oxidoreductase; Flavoprotein; NADP: FAD;
KM Mitochondrion; Transl. peptide.
FT TRANSIT 1 34
FT CHAIN 35 494
SEQUENCE 494 AA; 54362 MW; 5F07B37DFAA9525D CRC64;

Query Match 51.0%; Score 50.5; DB 1; Length 494;
Best Local Similarity 58.3%; Pred. No. 7.2;
Matches 7; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 1 RRMPMPMK-WP 11
Db 4 RCRMRWMSAMP 15

RESULT 7
ID Y945_MYCTU STANDARD; PRT; 253 AA.
AC P1564;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE OXIDOREDUCTASE RV0945 (EC 1.-.-.-).
GN RV0945 OR MT0971 OR MTCY10D7.29C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RC MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekela F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holtroyd S.,
RA Hovnsby T., Jagsels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skellern S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CDC 1551 / Oshkosh;
RC Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RC Peterson J., Deboy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
RC Kolonay J.F., Nelson W.C., Ormazabal L.A., Ermolaeva M.D., Salzberg S.L.,
RC Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.

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DR EMBL: Z79700: CAB02005.1; -
DR EMBL: AE006982; AAK45219.1; -
DR TIGR: MT0971; -
DR Tuberculin; RV0945; -
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PROSITE: PS00061; ADH_SHORT; 1.
KM Hypothetical protein; Oxidoreductase; Complete proteome.
FT ACT SITE 159 159
FT SITE BY SIMILARITY.
SEQUENCE 253 AA; 27138 MW; BAD937208842DA12 CRC64;

Query Match 50.0%; Score 49.5; DB 1; Length 253;
Best Local Similarity 70.0%; Pred. No. 5.3;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 4 PWWPKKPLI 13
Db 230 PWWPKA-PLV 238

RESULT 8
ID ADRO_HUMAN STANDARD; PRT; 491 AA.
AC P22570; Q13716;
DT 01-AUG-1991 (Rel. 19, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE NADPH:ADRENODOXIN OXIDOREDUCTASE, MITOCHONDRIAL PRECURSOR
DE (EC 1.18.1.2) (ADRENODOXIN REDUCTASE) (AR) (FERREDOXIN-NADP(+)
DE REDUCTASE)
GN FDXR OR ADAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89017146; PubMed=2845396;
RA Solish S.B., Picado-Leonard J., Morel Y., Kuhn R.W., Mohandas T.K.,
RA Hanukoglu I., Miller W.L.;
RT "Human adrenodoxin reductase: two mRNAs encoded by a single gene on
RT chromosome 1cen--7q25 are expressed in steroidogenic tissues."
RL Proc. Natl. Acad. Sci. U.S.A. 85:7104-7108(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=91046028; PubMed=2236061;
RA Lin D., Shi Y., Miller W.L.;
RT "Cloning and sequence of the human adrenodoxin reductase gene."
RL Proc. Natl. Acad. Sci. U.S.A. 87:8516-8520(1990).
-1- FUNCTION: SERVES AS THE FIRST ELECTRON TRANSFER PROTEIN IN ALL THE
CC MITOCHONDRIAL P450 SYSTEMS. INCLUDING CHOLESTEROL SIDE CHAIN
CC CLEAVAGE IN ALL STEROIDogenic TISSUES, STEROID 11-BETA
CC HYDROXYLATION IN THE ADRENAL CORTEX, 25-OH-VITAMIN D3-24
CC HYDROXYLATION IN THE KIDNEY, AND STEROL C-27 HYDROXYLATION IN THE
CC LIVER.
-1- CATALYTIC ACTIVITY: REDUCED ADRENODOXIN + NADP(+) = OXIDIZED
CC ADRENODOXIN + NADPH.
-1- COFACTOR: FAD.
-1- PATHWAY: CHOLESTEROL SIDE-CHAIN-CLEAVAGE SYSTEM.
-1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A SHORT FORM (SHOWN HERE) AND A
CC LONG FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE LONG FORM
CC REPRESENTS 10-20% OF ALL ADRENODOXIN REDUCTASE mRNA. AND SEEMS TO
CC BE INACTIVE.

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EMBL; X86031; CAAB0023.1; Cathelicidin.
DR InterPro; IPR001894; Cathelicidins; 1.
Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidins_1; 1.
DR PROSITE; PS00946; CATHELICIDINS_2; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
KW Antidiotic; Repeat; Amidation; Signal.
FT NON_TER 1 1
FT SIGNAL <1 13 POTENTIAL.
FT PROPEP 14 130 PROPENIN-1.
FT PEPTIDE 131 209 REMOVED IN MATURE FORM (POTENTIAL).
FT PROPEP 210 212 PYROLIDONE CARBOXYLIC ACID (BY
FT MOD_RES 14 14 SIMILARITY).
FT DISULFID 69 80 BY SIMILARITY.
FT DISULFID 91 108 BY SIMILARITY.
FT MOD_RES 209 209 AMIDATION (G-210 PROVIDE AMIDE GROUP)
(POTENTIAL).
DOMAIN 116 212 PRO-RICH.
DOMAIN 132 201 7 X 10 AA TANDEM REPEATS.
REPEAT 132 141 1.
REPEAT 142 151 2.
REPEAT 152 161 3.
REPEAT 162 171 4.
REPEAT 172 181 5.
REPEAT 182 191 6.
REPEAT 192 201 7.
SQ SEQUENCE 212 AA; 23956 MW; A31541AC9DDE423 CRC64;

QY 1 RRRPMWPKMKPLI 13
   11:111 11:
Db 113 KRPPWM---WPFL 122

Query Match          49.0%; Score 48.5; DB 1; Length 212;
Best Local Similarity 53.8%; Pred. No. 6;
Matches 7; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

RESULT 10
PF12_PIG STANDARD; PRT; 228 AA.
ID PF12_PIG
AC P51525;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PROPENIN-2 PRECURSOR (PF-2) (PR-2) (CL2) (PROPENIN-1 LIKE).
OS Sus scrofa (Pig).
SC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mamalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=94085623; PubMed=8262247;
RA Pungerecar J., Strkelj B., Kopitar G., Renko M., Lenarcic B.,
   Gubensek F., Turk V.;
RT "Molecular cloning of a putative homolog of proline/arginine-rich
   antibacterial peptides from porcine bone marrow.";
RL FEBS Lett. 336:284-288(1993).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=96105365; PubMed=7498526;
RA Zhao C., Ganz T., Lehrer R.I.;
RT "Structures of genes for two cathelin-associated antimicrobial
   peptides: propenin-2 and PR-39.";
RL FEBS Lett. 376:130-134(1995).
-i- FUNCTION: EXERTS ANTIMICROBIAL ACTIVITY. IT IS MORE EFFECTIVE
    AGAINST GRAM NEGATIVE BACTERIA THAN GRAM POSITIVE BACTERIA.
CC -1- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
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DR EMBL; X75438; CAA53188.1; -;
 DR EMBL; X89202; CAA61488.1; -;
 DR InterPro: IPR001894; Cathelicidin.
 DR Pfam: PF00666; Cathelicidins; 1.
 DR PROSITE: PS001838; Cathelicidin; 1.
 DR PROSITE: PS00946; Cathelicidins; 1.
 DR PROSITE: PS00947; Cathelicidins; 2; 1.
 KW Antibiotic; Repeat; Amidation; Signal.
 FT SIGNAL 1 29
 FT PROPEP 30 146
 FT PEPTIDE 147 225
 FT PROPEP 226 228
 FT MOD_RES 225 225
 FT DOMAIN 132 228
 FT DOMAIN 148 217
 FT REPEAT 148 157
 FT REPEAT 158 167
 FT REPEAT 168 177
 FT REPEAT 178 187
 FT REPEAT 188 197
 FT REPEAT 198 207
 FT REPEAT 208 217
 FT MOD_RES 30 30
 FT DISULFID 85 96
 FT DISULFID 107 124
 SQ SEQUENCE 228 AA; 25855 MW; 1EA4511FE35CC182 CRC64;

Query Match 49.0%; Score 48.5; DB 1; Length 228;
 Best local Similarity 53.8%; Pred. No. 6.4;
 Matches 7; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

OY 1 RRMPMPMKWPLI 13
 DB 129 RRFPWM--WPFL 138

RESULT 11
 ENV_OMVVS
 ID ENV_OMVVS STANDARD; PRT; 990 AA.
 AC P16899;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN).
 GN ENV.
 OS Ovine lentivirus (strain SA-OMV).
 OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11664;
 RX MEDLINE=90233989; PubMed=2158181;
 RA Querat G., Audoly G., Sonigo P., Vigne R.;
 RT "Nucleotide sequence analysis of SA-OMV, a visna-related ovine
 RT lentivirus: phylogenetic history of lentiviruses."; <http://www.isb-sib.ch/announce/>
 RT Virology 175:434-447(1990).
 CC CC
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CC EMBL; M34193; AAA6783.1; -;
 DR EMBL; M31646; AAA6817.1; -;
 DR PIR; G46335; G46335.
 DR HIV; M34193; ENV5OMVVSACG.
 DR InterPro: IPR000328; Env_Gp41.
 DR Pfam: PF00517; GP41; 1.
 KW Glycoprotein; Coat protein; Polypeptide; Transmembrane.
 FT PEPTIDE 1 101
 FT CHAIN 102 662
 FT CHAIN 663 990
 FT TRANSMEM 842 863
 FT CARBOHYD 141 141
 FT CARBOHYD 162 162
 FT CARBOHYD 207 207
 FT CARBOHYD 259 259
 FT CARBOHYD 299 299
 FT CARBOHYD 363 363
 FT CARBOHYD 386 386
 FT CARBOHYD 402 402
 FT CARBOHYD 413 413
 FT CARBOHYD 434 434
 FT CARBOHYD 438 438
 FT CARBOHYD 469 469
 FT CARBOHYD 474 474
 FT CARBOHYD 480 480
 FT CARBOHYD 490 490
 FT CARBOHYD 500 500
 FT CARBOHYD 514 514
 FT CARBOHYD 516 516
 FT CARBOHYD 526 526
 FT CARBOHYD 536 536
 FT CARBOHYD 542 542
 FT CARBOHYD 550 550
 FT CARBOHYD 560 560
 FT CARBOHYD 567 567
 FT CARBOHYD 703 703
 FT CARBOHYD 771 771
 FT CARBOHYD 778 778
 FT CARBOHYD 794 794
 SQ SEQUENCE 990 AA; 114498 MW; 279B816B55614F3 CRC64;

Query Match 48.5%; Score 48; DB 1; Length 990;
 Best local Similarity 50.0%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 RRMPMPMKWPL 12
 DB 174 QEWPMNTYHWP 185

RESULT 12
 ENV_CAEGV
 ID ENV_CAEGV STANDARD; PRT; 942 AA.
 AC P31627;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: SURFACE
 DE PROTEIN, TRANSMEMBRANE PROTEIN].
 GN ENV.
 OS Caprine arthritis encephalitis virus (strain 663) (CAEV).
 OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11662;
 RX MEDLINE=92015464; PubMed=1656067;
 RA Harwood W.G., Stem T.A.;
 RT "Structure and genetic variability of envelope glycoproteins of two
 RT antigenic variants of caprine arthritis-encephalitis lentivirus."; <http://www.isb-sib.ch/announce/>
 RT J. Virol. 65:5744-5750(1991).
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ID	ENV_VILV	STANDARD:	PRT:	982 AA.
AC	P03379;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN).			
GN	ENV.			
OS	Visna lentivirus (strain 1514).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_Taxid=11742;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8554938; PubMed=2410140;			
RA	Sonigo P., Aizon M., Staek K., Klatzmann D., Cole S., Danos O.,			
RA	Rezel E., Tioillais P., Haase A., Wain-Hobson S.;			
RT	"Nucleotide sequence of the visna lentivirus: relationship to the			
RT	AIDS virus.";			
RL	Cell 42:369-382(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86062965; PubMed=2824836;			
RA	Braun M.J., Clements J.E., Gonda M.A.;			
RT	"The visna virus genome: evidence for a hypervariable site in the env			
RT	gene and sequence homology among lentivirus envelope proteins.";			
Rb	J. Virol. 61:4046-4054(1987).			
CC	-----			
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CC	-----			
DR	EMBL; M10608; -; NOT_ANNOTATED_CDS.			
DR	EMBL; M51543; -; NOT_ANNOTATED_CDS.			
DR	EMBL; A15114; CA01216.1; -;			
DR	PIR; A03977; VCLJVS.			
DR	HIV; M10608; ENVSVLVCG.			
DR	InterPro; IPR000328; Env_GP41.			
DR	Pfam; PF00517; GP41; 1.			
KM	Glycoprotein; Coat protein; Polypeptide; Transmembrane.			
FT	PEPTIDE	1	100	
FT	CHAIN	101	656	LEADER PEPTIDE.
FT	CHAIN	657	982	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	TRANSMEM	835	851	TRANSMEMBRANE GLYCOPROTEIN.
FT	CARBOHYD	140	140	POTENTIAL.
FT	CARBOHYD	161	161	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	206	206	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	258	258	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	298	298	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	364	364	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	370	370	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	381	381	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	387	387	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	403	403	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	414	414	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	435	435	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	439	439	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	470	470	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	475	475	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	481	481	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	491	491	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	501	501	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	515	515	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	527	527	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	537	537	N-LINKED (GLCNAC. . .)	(POTENTIAL).			
FT	CARBOHYD	542	542	N-LINKED (GLCNAC. . .)	(POTENTIAL).			
FT	CARBOHYD	543	543	N-LINKED (GLCNAC. . .)	(POTENTIAL).			
FT	CARBOHYD	568	568	N-LINKED (GLCNAC. . .)	(POTENTIAL).			
FT	CARBOHYD	697	697	N-LINKED (GLCNAC. . .)	(POTENTIAL).			
FT	CARBOHYD	764	764	N-LINKED (GLCNAC. . .)	(POTENTIAL).			
FT	CARBOHYD	771	771	N-LINKED (GLCNAC. . .)	(POTENTIAL).			
FT	CARBOHYD	787	787	N-LINKED (GLCNAC. . .)	(POTENTIAL).			
FT	CARBOHYD	821	821	N-LINKED (GLCNAC. . .)	(POTENTIAL).			
FT	VARIANT	12	12	T -> M (IN REF. 2).				
FT	VARIANT	118	118	S -> N (IN REF. 2).				
FT	VARIANT	283	283	K -> R (IN REF. 2).				
FT	VARIANT	640	641	ER -> AQ (IN REF. 2).				
FT	VARIANT	645	645	R -> K (IN REF. 2).				
SO	SEQUENCE	982 AA;	113978 MW;	7D7BBA6E22BF53F CRC64;				
DQ	3 WPMWPKMPL	12						
	:							
Db	175 WPMWTYHMP	184						
Query Match	Best Local Similarity	47.5%;	Score 47;	DB 1;	Length 982;			
Matches	6; Conservative	1;	Mismatches	3;	Indels	0;	Gaps	0;
RESULT	15							
ID	ENV_VILVK	STANDARD;	PRT;	983 AA.				
AC	P35954;							
DT	01-JUN-1994 (Rel. 29, Created)							
DT	01-JUN-1994 (Rel. 29, Last sequence update)							
DT	20-AUG-2001 (Rel. 40, Last annotation update)							
DE	ENV POLYPEPTIDE PRECURSOR (COAT POLYPEPTIDE).							
GN	ENV.							
OS	Visna lentivirus (strain KV1772).							
OC	Vituses; Retroid viruses; Retroviridae; Lentivirus.							
OX	NCBI_TaxID=36374;							
RA	[1]							
RX	SEQUENCE FROM N.A.							
RA	MEDLINE=93174981; PubMed=8382414;							
RA	Andresson O.S., Elser J.E., Tobin G.J., Greenwood J.D., Gonda M.A.,							
RA	Georgsson G., Andresdottir V., Benediktssdottir E., Carlsdottir H.M.,							
RA	Maentylae E.O., Rathar B., Palsson P.A., Casey J.W., Petursson G.;							
RT	*Nucleotide sequence and biological properties of a pathogenic							
RT	proviral molecular clone of neurotropic visna virus.";							
RL	Virology 193:89-105(1993).							
CC	-----							
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CC	-----							
DR	EMBL; S55323; AAB25463.1; -.							
DR	EMBL; L06906; AAA48362.1; -.							
DR	PIR; E45390; EA5390.							
DR	InterPro; IPR000326; Env-CP41.							
DR	Ftm; PF00517; GP41; 1.							
KW	Glycoprotein; Coat protein; Polypeptide; Transmembrane.							
FT	PEPTIDE	1	100	LEADER PEPTIDE.				
FT	CHAIN	101	656	EXTERIOR MEMBRANE GLYCOPROTEIN.				
FT	CHAIN	657	983	TRANSMEMBRANE GLYCOPROTEIN.				
FT	TRANSMEM	836	852	POTENTIAL.				
FT	CARBOHYD	140	140	N-LINKED (GLCNAC. . .)	(POTENTIAL).			
FT	CARBOHYD	161	161	N-LINKED (GLCNAC. . .)	(POTENTIAL).			
FT	CARBOHYD	206	206	N-LINKED (GLCNAC. . .)	(POTENTIAL).			
FT	CARBOHYD	258	258	N-LINKED (GLCNAC. . .)	(POTENTIAL).			
FT	CARBOHYD	298	298	N-LINKED (GLCNAC. . .)	(POTENTIAL).			
FT	CARBOHYD	364	364	N-LINKED (GLCNAC. . .)	(POTENTIAL).			
FT	CARBOHYD	381	381	N-LINKED (GLCNAC. . .)	(POTENTIAL).			

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FT CAROHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 414 414 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 439 439 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 470 470 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 491 491 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 501 501 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 527 527 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CAROHYD 568 568 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 697 697 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 765 765 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 772 772 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 788 788 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 822 822 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 900 900 R -> H (IN REF. 1; AAA48362).
SQ SEQUENCE 983 AA: 113939 MM: E03BCC254EA78268 CRC64;
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Query Match 47.5%; Score 47; DB 1; Length 983;
Best Local Similarity 60.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 3 WPMWPMKMP 12
111 : 111
Db 175 WPMWPMKMP 184
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Search completed: January 30, 2002, 11:52:22
Job time: 201 sec